



SEQUENCE LISTING

<110> McKeon, F.
Kayako, K.
Ryeom, S.

<120> CALCIPRESSINS: ENDOGENOUS INHIBITORS OF CALCINEURIN,
USES AND REAGENTS RELATED THERETO

<130> HMV-048.01

<140> 09/575,580

<141> 2000-05-22

<150> 60/135,431

<151> 1999-05-21

<150> 60/161,195

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<170> PatentIn Ver. 2.1

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<211> 2484

<212> DNA

<213> Homo sapiens

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<212> DNA
<213> Mus musculus

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 <211> 198
 <212> PRT
 <213> Mus musculus

<400> 4
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 35 40 45
 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
 50 55 60
 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65 70 75 80
 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
 85 90 95
 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110
 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
 115 120 125
 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
 130 135 140
 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
 145 150 155 160
 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
 165 170 175
 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
 180 185 190
 Thr Pro Ile His Leu Ser
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<210> 5
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 <213> Mus musculus

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 35 40 45
 Leu Thr Asp Phe Ser Asp Leu Pro Asn Ser Leu Phe Ala Cys Asn Val
 50 55 60
 His Gln Ser Val Phe Glu Glu Glu Glu Ser Lys Glu Lys Phe Glu Gly
 65 70 75 80
 Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe Lys Ser
 85 90 95
 Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala Ala Arg
 100 105 110
 Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Pro
 115 120 125
 Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu
 130 135 140
 His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro
 145 150 155 160
 Ser Ser Pro Ser Val Gly Trp Lys Pro Ile Ser Asp Ala Thr Pro Val
 165 170 175
 Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu
 180 185 190
 Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val
 195 200 205
 His Val Cys Asp Ser Asp Met Glu Arg Glu Glu Asp Pro Lys Thr Ser
 210 215 220
 Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly Leu Pro Pro Phe
 225 230 235 240
 Gly His

<210> 6
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 6
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 Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
 35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
 50 55 60
 Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
 65 70 75 80
 Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
 85 90 95
 Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
 100 105 110
 Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
 115 120 125
 Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
 130 135 140
 Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
 145 150 155 160
 Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
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 Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
 180 185 190

<210> 7
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 7
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 Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn Phe
 20 25 30
 Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr
 35 40 45
 Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His
 50 55 60
 Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu
 65 70 75 80
 Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp
 85 90 95
 Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu
 100 105 110

Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro
 115 120 125
 Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu
 130 135 140
 Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr
 145 150 155 160
 Arg Arg Pro Glu Tyr Thr Pro Ile His Leu
 165 170

<210> 8
 <211> 197
 <212> PRT
 <213> *Cricetulus griseus*

<400> 8
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 1 5 10 15
 Val Ala Asn Gly Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
 20 25 30
 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
 35 40 45
 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
 50 55 60
 Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65 70 75 80
 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
 85 90 95
 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110
 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
 115 120 125
 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
 130 135 140
 Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
 145 150 155 160
 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg Met
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 Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
 180 185 190
 Pro Ile His Leu Ser
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<210> 9
<211> 207
<212> PRT
<213> Caenorhabditis elegans
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| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ser | Leu | Ile | Ser | Thr | Val | Ser | Ser | Lys | Asp | Asp | Leu | Pro | Asn | Ala | Ile | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ile | Val | Thr | Gln | Val | Pro | Glu | Asp | Val | Phe | Asp | Asn | Lys | Gln | Asp | Lys | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ala | Asn | Phe | Ser | Ser | Leu | Phe | Thr | Gln | Ile | Glu | Lys | Asp | Ile | His | Phe | |
| | 50 | | | | | 55 | | | | | | 60 | | | | |
| Asp | Phe | Leu | Arg | Ser | Phe | Arg | Arg | Val | Arg | Val | Ile | Phe | Ser | Ser | Pro | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Glu | Asn | Ala | Thr | Ala | Ala | Lys | Leu | Ile | Val | Gln | Gly | Phe | Ser | Phe | Lys | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Gly | His | Glu | Leu | Lys | Ala | Phe | Phe | Ala | Gln | Arg | Ile | Tyr | Met | Ser | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Asn | Ser | Gln | Met | Leu | Ser | Pro | Pro | Pro | Leu | Glu | Lys | Gln | Phe | Leu | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ser | Pro | Pro | Cys | Ser | Pro | Pro | Val | Gly | Trp | Glu | Gln | Thr | Lys | Asp | Met | |
| | 130 | | | | | 135 | | | | | | 140 | | | | |
| Pro | Pro | Val | Val | Cys | Asn | Phe | Asp | Leu | Met | Ala | Arg | Leu | Ala | Ser | Phe | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ala | Ile | Asp | Glu | Lys | Tyr | Glu | Val | His | Asn | Gly | Asp | Glu | Leu | Thr | Pro | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Ala | Ile | Ile | Val | His | Pro | Cys | Glu | Thr | Pro | Ile | Asp | Val | Pro | Ser | Ala | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Ile | Glu | Met | Pro | Arg | Thr | Pro | Arg | Pro | Ser | Ser | Pro | Cys | Glu | Gln | | |
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<210> 10
<211> 211
<212> PRT
<213> Saccharomyces cerevisiae
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Asp Ile Val Asp Asn Asp Asn Val Glu Arg Ile Gln Val Trp Leu Ser  
          20              25              30
```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Ile | Leu | Arg | Lys | Phe | Gln | Ile | Asn | Glu | Asn | Glu | Pro | Leu | Gln |
| 35 | | | | | | 40 | | | 45 | | | | | | |
| Leu | Ile | Ile | Leu | Lys | Arg | Phe | Lys | Arg | Ile | Leu | Leu | Ile | Cys | Pro | Ser |
| 50 | | | | | | 55 | | | 60 | | | | | | |
| His | Asp | Ile | Ser | Gln | His | Val | Met | Asp | Ala | Ser | Arg | Ala | Leu | Glu | Met |
| 65 | | | 70 | | | | | | 75 | | | 80 | | | |
| Glu | Asn | Phe | Asn | Phe | Ser | Tyr | Ser | Leu | Gln | Asp | Gly | Gln | Arg | Asn | Leu |
| | | | 85 | | | | | | 90 | | | 95 | | | |
| Thr | Lys | Gln | Tyr | Leu | Lys | Val | Pro | Glu | Ser | Glu | Lys | Met | Phe | Leu | Ile |
| | | | 100 | | | 105 | | | | | | 110 | | | |
| Ser | Pro | Pro | Ala | Ser | Pro | Pro | Pro | Glu | Phe | Asp | Phe | Ser | Lys | Cys | Glu |
| 115 | | | | | | 120 | | | 125 | | | | | | |
| Asp | Ala | Pro | Gln | Arg | His | Ile | Gln | Ser | His | Ile | Gln | Gln | Asp | Gln | Gln |
| 130 | | | | | | 135 | | | 140 | | | | | | |
| Gln | Arg | Leu | Glu | Ala | Ser | Gln | Leu | Leu | Pro | Asn | Asn | Pro | Asp | Lys | Asn |
| 145 | | | 150 | | | | | | 155 | | | 160 | | | |
| Asn | Asn | Gly | Thr | Phe | Thr | Leu | Leu | Lys | Ser | Lys | Val | Gly | Ala | Ile | Thr |
| | | | 165 | | | | | | 170 | | | 175 | | | |
| Ile | Asp | Arg | Cys | Pro | Thr | Asn | Asp | Gly | Asn | Gly | Gln | Met | Gln | Leu | Ala |
| | | | 180 | | | 185 | | | 190 | | | | | | |
| Asp | His | Val | Lys | Thr | Ala | Phe | Pro | Pro | Lys | Ser | Ile | Phe | Asp | Thr | Asp |
| 195 | | | | | | 200 | | | 205 | | | | | | |
| Asp | Asp | Asp | | | | | | | | | | | | | |
| 210 | | | | | | | | | | | | | | | |

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<210> 11
<211> 163
<212> PRT
<213> Schizosaccharomyces pombe
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<400> 11
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                20                      25                      30

Leu Gly Lys Val Leu Ala Ser Tyr Asn Asp Lys Ala Val Glu Glu Asp
      35                      40                      45

Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val
    50                      55                      60

His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser
  65                70                75                80

```


[illegible]

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<210> 12
<211> 8
<212> PRT
<213> Homo sapiens
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```
<400> 12
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```

```
<210> 13
<211> 11
<212> PRT
<213> Homo sapiens
```

```
<400> 13
Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro
  1             5             10
```

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<210> 14
<211> 16
<212> PRT
<213> Homo sapiens
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<400> 14
Glu Arg Met Lys Arg Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro
1 5 10 15

```
<210> 15
<211> 14
<212> PRT
<213> Homo sapiens
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```
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      1                      5                      10
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<210> 16
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 16
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 1 5 10

<210> 17
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 17
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 1 5 10

<210> 18
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 18
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 1 5 10

<210> 19
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 19
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 1 5 10

<210> 20
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 20
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 1 5 10

<210> 21
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 21

Pro Lys Pro Lys Ile Asn Gln Thr Arg Arg Pro Gly Leu Pro

1

5

10

<210> 22

<211> 724

<212> DNA

<213> Mus musculus

<400> 22

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ttccagttgt tcaagagctt tcgcagagtg aggatcaact tcagcaagcc cgaggctgcg 300
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<210> 23

<211> 958

<212> DNA

<213> Mus musculus

<400> 23

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agccagtcag acctctgtag cagcgaccag gaggaggaag aggagatggt cttcggtgaa 240
aatgaggacg gactggaaga gatgatggac ctaagtgacc tgcccacctc actctttgct 300
tgcagtgtcc atgaagcagt gtttgaggtc caagagcaaa aggagagggt tgaggccctg 360
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<211> 3717

<212> DNA

<213> Mus musculus

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<212> PRT

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<220>

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<210> 29

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<223> Description of Artificial Sequence: calcineurin
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Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu
  1             5             10

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<210> 33
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pH-dependent
 membrane-binding internalizing peptide

<220>
 <221> SITE
 <222> (1)
 <223> Xaa=preferably a unique residue, such as Cys or
 Lys, that facilitates chemical conjugation of the

internalizing peptide to a targeting protein
conjugate

<220>

<221> SITE

<222> (2)..(3)

<223> Xaa=residues selected to modulate the affinity of
the internalizing peptide for different membranes

<400> 33

Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
1 5 10 15

Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25 30

<210> 34

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide
substrate

<400> 34

Gly Asn Ala Ala Ala Arg Arg
1 5

<210> 35

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (4)..(75)

<220>

<223> Description of Artificial Sequence: synthetic
construct

<400> 35

cat atg ggt ggc tgc cgt ggc gat atg ttc ggt tgc ggt gct cct cca 48
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro
1 5 10 15

aaa aag aag aga aag gta gct gga ttc 75
Lys Lys Lys Arg Lys Val Ala Gly Phe
20

<210> 36
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<400> 36
 Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys
 1 5 10 15
 Lys Lys Arg Lys Val Ala Gly Phe
 20

<210> 37
 <211> 225
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<220>
 <221> CDS
 <222> (4)..(225)

<400> 37
 cat atg gag cca gta gat cct aga cta gag ccc tgg aag cat cca gga 48
 Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly
 1 5 10 15
 agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc 96
 Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys
 20 25 30
 ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat 144
 Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr
 35 40 45
 ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag 192
 Gly Arg Lys Lys Arg Arg Gln Arg Arg Pro Pro Gln Gly Ser Gln
 50 55 60
 act cat caa gtt tct cta agt aag caa gga ttc 225
 Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe
 65 70

<210> 38
 <211> 74

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic construct

<400> 38

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
50 55 60

His Gln Val Ser Leu Ser Lys Gln Gly Phe
65 70

<210> 39

<211> 912

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic construct

<220>

<221> CDS

<222> (4)..(912)

<400> 39

cat atg acc tct cgc cgc tcc gtg aag tcg ggt ccg cgg gag gtt ccg 48
Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro
1 5 10 15

cgc gat gag tac gag gat ctg tac tac acc ccg tct tca ggt atg gcg 96
Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala
20 25 30

agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca 144
Ser Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr
35 40 45

cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg 192
Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser
50 55 60

gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg 240
Asp Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro
65 70 75

| | |
|---|-----|
| gag gtc ccc cgg acg cgg cgt ccc gtt tcc ggg gcg gtt ttg tcc ggc | 288 |
| Glu Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly | |
| 80 85 90 95 | |
| ccg ggg cct gcg cgg gcg cct ccg cca ccc gct ggg tcc gga ggg gcc | 336 |
| Pro Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala | |
| 100 105 110 | |
| gga cgc aca ccc acc acc gcc ccc cgg gcc ccc cga acc cag cgg gtg | 384 |
| Gly Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val | |
| 115 120 125 | |
| gcg act aag gcc ccc gcg gcc ccg gcg gcg gag acc acc cgc ggc agg | 432 |
| Ala Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg | |
| 130 135 140 | |
| aaa tcg gcc cag cca gaa tcc gcc gca ctc cca gac gcc ccc gcg tcg | 480 |
| Lys Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser | |
| 145 150 155 | |
| acg gcg cca acc cga tcc aag aca ccc gcg cag ggg ctg gcc aga aag | 528 |
| Thr Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys | |
| 160 165 170 175 | |
| ctg cac ttt agc acc gcc ccc cca aac ccc gac gcg cca tgg acc ccc | 576 |
| Leu His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro | |
| 180 185 190 | |
| cgg gtg gcc ggc ttt aac aag cgc gtc ttc tgc gcc gcg gtc ggg cgc | 624 |
| Arg Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg | |
| 195 200 205 | |
| ctg gcg gcc atg cat gcc cgg atg gcg gcg gtc cag ctc tgg gac atg | 672 |
| Leu Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met | |
| 210 215 220 | |
| tcg cgt ccg cgc aca gac gaa gac ctc aac gaa ctc ctt ggc atc acc | 720 |
| Ser Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr | |
| 225 230 235 | |
| acc atc cgc gtg acg gtc tgc gag ggc aaa aac ctg ctt cag cgc gcc | 768 |
| Thr Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala | |
| 240 245 250 255 | |
| aac gag ttg gtg aat cca gac gtg gtg cag gac gtc gac gcg gcc acg | 816 |
| Asn Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr | |
| 260 265 270 | |
| gcg act cga ggg cgt tct gcg gcg tcg cgc ccc acc gag cga cct cga | 864 |
| Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg | |
| 275 280 285 | |
| gcc cca gcc cgc tcc gct tct cgc ccc aga cgg ccc gtc gag gaa ttc | 912 |
| Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe | |
| 290 295 300 | |

```
<210> 40
<211> 303
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: synthetic
construct

| | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> | 40 | | | | | | | | | | | | | | | |
| Met | Thr | Ser | Arg | Arg | Ser | Val | Lys | Ser | Gly | Pro | Arg | Glu | Val | Pro | Arg | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Asp | Glu | Tyr | Glu | Asp | Leu | Tyr | Tyr | Thr | Pro | Ser | Ser | Gly | Met | Ala | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Pro | Asp | Ser | Pro | Pro | Asp | Thr | Ser | Arg | Arg | Gly | Ala | Leu | Gln | Thr | Arg | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ser | Arg | Gln | Arg | Gly | Glu | Val | Arg | Phe | Val | Gln | Tyr | Asp | Glu | Ser | Asp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Tyr | Ala | Leu | Tyr | Gly | Gly | Ser | Ser | Ser | Glu | Asp | Asp | Glu | His | Pro | Glu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Val | Pro | Arg | Thr | Arg | Arg | Pro | Val | Ser | Gly | Ala | Val | Leu | Ser | Gly | Pro | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Gly | Pro | Ala | Arg | Ala | Pro | Pro | Pro | Pro | Ala | Gly | Ser | Gly | Gly | Ala | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Arg | Thr | Pro | Thr | Thr | Ala | Pro | Arg | Ala | Pro | Arg | Thr | Gln | Arg | Val | Ala | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Thr | Lys | Ala | Pro | Ala | Ala | Pro | Ala | Ala | Glu | Thr | Thr | Arg | Gly | Arg | Lys | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Ser | Ala | Gln | Pro | Glu | Ser | Ala | Ala | Leu | Pro | Asp | Ala | Pro | Ala | Ser | Thr | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Ala | Pro | Thr | Arg | Ser | Lys | Thr | Pro | Ala | Gln | Gly | Leu | Ala | Arg | Lys | Leu | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| His | Phe | Ser | Thr | Ala | Pro | Pro | Asn | Pro | Asp | Ala | Pro | Trp | Thr | Pro | Arg | |
| | | | 180 | | | | 185 | | | | | | 190 | | | |
| Val | Ala | Gly | Phe | Asn | Lys | Arg | Val | Phe | Cys | Ala | Ala | Val | Gly | Arg | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Ala | Ala | Met | His | Ala | Arg | Met | Ala | Ala | Val | Gln | Leu | Trp | Asp | Met | Ser | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Arg | Pro | Arg | Thr | Asp | Glu | Asp | Leu | Asn | Glu | Leu | Leu | Gly | Ile | Thr | Thr | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | |
| Ile | Arg | Val | Thr | Val | Cys | Glu | Gly | Lys | Asn | Leu | Leu | Gln | Arg | Ala | Asn | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
 260 265 270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala
 275 280 285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe
 290 295 300

<210> 41
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<220>
 <221> CDS
 <222> (4)..(120)

<400> 41
 cat atg gac gtc gac gcg gcc acg gcg act cga ggg cgt tct gcg gcg 48
 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala
 1 5 10 15

tcg cgc ccc acc gag cga cct cga gcc cca gcc cgc tcc gct tct cgc 96
 Ser Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg
 20 25 30

ccc aga cgg ccc gtc gag gaa ttc 120
 Pro Arg Arg Pro Val Glu Glu Phe
 35

<210> 42
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
 construct

<400> 42
 Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
 1 5 10 15

Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
 20 25 30

Arg Arg Pro Val Glu Glu Phe
 35

<210> 43
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 43
 aggaggtgga tctgc

15

<210> 44
 <211> 6
 <212> PRT
 <213> Mus musculus

<400> 44
 Glu Arg Met Arg Arg Pro
 1 5

<210> 45
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus
 sequence

<400> 45
 Glu Arg Met Pro Pro Arg Arg Asp
 1 5

<210> 46
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: cross-species
 conserved motif

<220>
 <221> MOD_RES
 <222> (6)
 <223> Variable amino acid

<400> 46
 Leu Ile Ser Pro Pro Xaa Ser Pro
 1 5

<210> 47
 <211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist
peptide fragment

<220>
<221> MOD_RES
<222> (4)
<223> Any amino acid residue other than Ser or Thr

<400> 47
Arg Arg Pro Xaa
1

<210> 48
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist
peptide fragment

<220>
<221> MOD_RES
<222> (4)
<223> Ala, Gly or Glu

<400> 48
Arg Arg Pro Xaa
1

<210> 49
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin antagonist
peptide fragment

<400> 49
Arg Arg Pro Glu
1